P2 18: Distribution and genetic diversity of Peste des Petits Ruminants virus in Mali

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Peste de Petits Ruminants (PPR) is a highly contagious infectious disease of sheep and goats. The disease is endemic in Africa, Middle East and Asia (Libeau, Diallo et al. 2014). PPR has been classified among diseases that must be notified to the World Organization for Animal Health (OIE). The causal agent of the disease is a virus, peste-des-petitsruminants virus (PPRV). The genome of the PPRV encodes for two non-structural proteins C and V and six structural proteins: nucleoprotein (N), phosphoprotein (P), matrix protein (M) fusion protein (F) hemagglutinin protein (H) and viral RNA-dependant polymerase (L) (Bailey, Banyard et al. 2005). Based on the partial sequences of the N gene, PPRV has been classified into four genetically distinct lineages (I, II, III, and IV) (Banyard et al., 2010). The PPRV circulating in Asian and the Middle East belong to the lineage III and IV. But in Africa, all the four lineages are present. Until now, the PPRV present in West Africa belong to the lineage I and II (Banyard et al., 2010). The lineage II is thought to have replace lineage I in its historical distribution in West Africa (Banyard et al. 2010). In this study, we characterized the PPR virus from five different regions of Mali (Bamako, Ségou, Kayes, Sikasso and Mopti). The samples have been collected in 1999, 2014, 2015, 2016 and 2017. We analyzed the partial N-gene sequence in comparison with other viruses from Africa. The phylogenetic tree that we obtain shows that the samples recently collected in 2017 in Mopti belong to the lineage IV and are very closely related to the lineage IV of Nigeria (Woma et al. 2015). All the other samples belong to the lineage I and II. Our results represent the first confirmations of the persistence of lineage I and of the presence of lineage IV in a region dominated by lineage II. We also sequenced the full genome of the PPR virus of those samples. The phylogeographic and phylogenetic analysis were performed to assess the persistence of the lineage I and II in Mali and the spread of PPRV circulating from Eastern Africa in Mali.

References

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